

## Exhibit B

### **Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/783,669**

1. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO: 4; and
  - (b) hybridizes under highly stringent conditions to the complement of the nucleotide sequence of SEQ ID NO: 3 [or the complement thereof].
- 2.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:4.
- 3.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:2.
- 4.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:6.
- 5.(New) A cell comprising the expression vector of Claim 2.
- 6.(New) A cell comprising the expression vector of Claim 3.
- 7.(New) A cell comprising the expression vector of Claim 4.

Exhibit B  
Seq Id No:1 versus human genome

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## Paracel BLAST Results

Help

MEGABLAST 1.2.3-Paracel [2001-11-20]

**Reference:**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
"A greedy algorithm for aligning DNA sequences",  
J Comput Biol 2000; 7(1-2):203-14.

**Database:** Homo\_sapiens.latestgp.masked.fa  
33,840 sequences; 200,810,911,373 total letters

**Query=** hGPR\_32 = Seq Id No:1  
(813 letters)

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Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

AC027026.10.1.155376	1138	0.0
AC023078.9.1.163718	238	4e-60
AC107948.7.1.156839	216	2e-53
AC090099.14.1.172939	216	2e-53
AC103974.6.1.189230	212	3e-52

>AC027026.10.1.155376  
Length = 155376

Score = 1138 bits (574), Expect = 0.0  
Identities = 574/574 (100%)  
Strand = Plus / Minus

Query: 1 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60  
|||||  
Sbjct: 31187 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 31128

Query: 61 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctgatccttttcatt 120  
|||||  
Sbjct: 31127 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctgatccttttcatt 31068

Query: 121 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180  
|||||  
Sbjct: 31067 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 31008

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240  
|||||  
Sbjct: 31007 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 30948

Query: 241 ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 300  
|||||  
Sbjct: 30947 ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 30888

Query: 301 ttccctagcttcttccaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360  
|||||

Sbjct: 30887 ttccctagctttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 30828

Query: 361 agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420  
|||||

Sbjct: 30827 agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 30768

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|||||

Sbjct: 30767 cgccccagacacctgtcagcgggtcggtgtgtgtcctgctctgggccctgtccctactgctg 30708

Query: 481 agcatcttggaagggaagttctgtggcttcttatttagtgatgggtgactctgggtgggtgt 540  
|||||

Sbjct: 30707 agcatcttggaagggaagttctgtggcttcttatttagtgatgggtgactctgggtgggtgt 30648

Query: 541 cagacatttgatttcatcactgcagcgtggctga 574  
|||||

Sbjct: 30647 cagacatttgatttcatcactgcagcgtggctga 30614

Score = 442 bits (223), Expect = e-121  
Identities = 230/232 (99%), Gaps = 1/232 (0%)  
Strand = Plus / Minus

Query: 582 attcatggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccag 641  
|||||

Sbjct: 30606 attcatggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccag 30547

Query: 642 gggctctgccactgaccaggctgtacctgaccatcctgctcacagtgcctgggtgttcctcct 701  
|||||

Sbjct: 30546 gggctctgccactgaccaggctgtacctgaccatcctgctcacagtgcctgggtgttcctcct 30487

Query: 702 ctgcggcctgccctttggcattcagtggttcctaataattatggatctggaaggattctga 761  
|||||

Sbjct: 30486 ctgcggcctgccctttggcattcagtggttcctaataattatggatctggaaggattctga 30427

Query: 762 tgtcttattttggcatattcatccaagtttcagttgtcctgtcatctcttaa 813  
|||||

Sbjct: 30426 tgtcttattttgtcatattcatcc-agtttcagttgtcctgtcatctcttaa 30376

>AC023078.9.1.163718  
Length = 163718

Score = 238 bits (120), Expect = 4e-60  
Identities = 212/242 (87%), Gaps = 4/242 (1%)  
Strand = Plus / Minus

Query: 335 cctaccttgaggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcc 394  
|||||

Sbjct: 71224 cctactttgcaggcctgagctttctgagtgccgtgagcaccgagcgctgcctgtccgtcc 71165

Query: 395 tgtggcccatctggtatcgctgccgccccagacacctgtcagcggtcgtgtgtgtcc 454  
|||||

Sbjct: 71164 tgtggcccatctggtaccgctgccaccgccccacacctgtcagcggtggtgtgtgtcc 71105

Query: 455 tgctctggggccctgtccctactgctgagcatcttgaag-ggaagttctgtggcttctta 513  
|||||

Sbjct: 71104 tgctctggggccctgtccctgctgaggagcatcctgga-gtggatgttatgtggcttctg 71046

Query: 514 tttagtgatggtgactctggttggtgtcagacatttgatttcactg-cagcggtggct 572  
|| |||

Sbjct: 71045 ttcagtgggtgctgattctgcttggtgtcaaacatcagatttcactcacagtc-gcgtggct 70987

Query: 573 ga 574  
||

Sbjct: 70986 ga 70985

Score = 222 bits (112), Expect = 3e-55  
Identities = 206/236 (87%), Gaps = 7/236 (2%)  
Strand = Plus / Minus

Query: 344 caggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgtggcca 403  
|||||

Sbjct: 24330 caggcctgagcatgctgagcaccatcagcaccgagcaccgctgcctgtccgtcctgtggcca 24271

Query: 404 tctggtatc-gctgccgccccagacacctgtcagcggtcgtgtgtgtcctgctctgg 462  
|||||

Sbjct: 24270 tctggta-ctgctgccactgccccacacctgtcagcggtcatgtgtgtcctgctctgg 24212

Query: 463 gccctgtccctactgctgagcatcttgaag-ggaagttctgtggcttcttatttagtga 521  
|||||

Sbjct: 24211 gccctgtccctgttgagagcatcctgga-gtggatgttctgtagcttctgtttagtga 24153

Query: 522 tgggtgactctggt--t-ggtgtcagacatttgatttcactgagcggtggctga 574  
|| |||

Sbjct: 24152 tgttgactctgataattggtgtcaaataattagatttcctcactgctgtgtggctga 24097

Score = 212 bits (107), Expect = 3e-52  
Identities = 214/249 (85%), Gaps = 4/249 (1%)  
Strand = Plus / Minus

Query: 313 ttcaccactgtgatgacctgtgc-ctaccttgaggcctgagcatgctgagcaccgtcag 371  
|||||

Sbjct: 963 ttcaccactgtgatgacct-ttctctactttacaggcctgagcatgctgggctccatcag 905

Query: 372 caccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgcccagaca 431  
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 904 caccaagcactgcctgtccatcctgtggcccatctagtaccgctgccaccacccacaca 845

Query: 432 cctgtcagcggcgtgtgtgtgtcctgtctgtggccctgtccctactgctgagcatcttga 491  
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 844 cctgtcagcagtc--gtgtgtcctgtctgtggccctgtccctgctgcagagcatcctga 787

Query: 492 aggggaagttctgtggcttcttatttagtgatggtgactctggttggtgtcagacatttga 551  
| ||| ||||| ||||| ||| ||||| || ||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 786 atggatgttctgtggcttctgtctagtgggtgctgattctgtttggtgtgaaacatcaga 727

Query: 552 tttcatcac 560  
|||||  
Sbjct: 726 tttcatcac 718

Score = 190 bits (96), Expect = 9e-46  
Identities = 208/244 (85%), Gaps = 7/244 (2%)  
Strand = Plus / Minus

Query: 320 ctgtgatgacctgtgcctacctt-gcaggcctgagcatgctgagcaccgtcagcaccgag 378  
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 47852 ctgtgatgacctttcccta-cttggcaggcctgaatattctgagtgccatgagcaccaag 47794

Query: 379 cgctgcctgtccgtcctgtggcccatctggtatcgctgccgcccagacacctgtca 438  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 47793 cgctgcctgtcaatcctgtggcccatctggtaacgctgccgccacccacacacctgtca 47734

Query: 439 gcggtcgtgtgtgtcctgtctgtggccctgtccctactgct-gagcatcttgaag-gga 496  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 47733 acggtcgtgtgtgtcctgtctgtggccctgtccctgctg-tagagcatcctgga-gtgga 47676

Query: 497 agttctgtggcttcttatttagtgatggtgactctggttggtgtcagacatttgatttca 556  
||||| ||| ||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 47675 tgttctgtgactccctgttttagtgatgctgattctgtttggtgtcaaacatcagatt-ca 47617

Query: 557 tcac 560  
|||  
Sbjct: 47616 tcac 47613

Score = 186 bits (94), Expect = 1e-44  
Identities = 190/221 (85%), Gaps = 6/221 (2%)  
Strand = Plus / Minus

Query: 344 caggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgtggcca 403  
||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 109133 caggcctgagcttctgagtccatgagcaccgagcgctgcctgtgcgtcctgtggcca 109074

Query: 404 tctggtatcgctgccgcccgc--agacacctgtcagcggtcgtgtgtgtcctgctctg 461  
|||||  
Sbjct: 109073 tctggtaccgctgcctcctccccccacacacctgtcagcggtcgtgtgtgtcctgctttg 109014

Query: 462 ggccctgtccctactgctgagcatcttgaaggaa-gttctgtggcttcttatttagtg 520  
|||||  
Sbjct: 109013 ggccctgtccctactgcggagcatcctgga-gtgaatgttctgtgacttctgttttagtg 108955

Query: 521 atggtgactctggttggtgtcagac-atttgatttcatcac 560  
||| ||| |||  
Sbjct: 108954 atgctgattctatttggtgtca-accatcagatttcatcac 108915

Score = 170 bits (86), Expect = 9e-40  
Identities = 194/229 (84%), Gaps = 6/229 (2%)  
Strand = Plus / Minus

Query: 335 cctaccttgaggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcc 394  
|||||  
Sbjct: 93453 cctaccttgcaagcctgagctttctaagcgccatgagcaccgagcgctgcctgtacgtcc 93394

Query: 395 tgtggcccatctggtatcgctgccgcccgc--ccag-acacctgtcagcggtcgtgtgtgt 452  
|||||  
Sbjct: 93393 tgtggcccatctggttagcgctgccgccccgcacctacacctgtcagcggtcgtgtgtgt 93334

Query: 453 cctgctctgggccctgtccctactgctgagcatcttgaag-ggaagtt-ctgtggcttc 510  
| |||||  
Sbjct: 93333 catgctctgggccctgtctctgctgaggcgctcctgga-gtgga-gtttctgtgacttc 93276

Query: 511 ttatttagtgatggtgactctggttggtgtcagacatttgatttcatca 559  
| |||||  
Sbjct: 93275 ctgttttagtggtgctgattctgtttggtgttaaacatcagatttcatca 93227

Score = 161 bits (81), Expect = 8e-37  
Identities = 142/162 (87%), Gaps = 2/162 (1%)  
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtctggccctgctgggtcaggatcctctgtggctccaggg-gt 645  
|||||  
Sbjct: 70972 tggttctctgtgggtccagcctggctcctgctgatcaggattctctgtggatcccgaaga 70913

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgtgtggttctcctctgc 705  
| |||  
Sbjct: 70912 -taccgctgaccaggctgtacctgaccatcctgctcacagtactggttctcctcctctgt 70854

Query: 706 ggccctgccctttggcattcagtgggttcctaataattatggatc 747

|||||  
Sbjct: 70853 ggcctgccctttggcattcagtttttctatttttatggatc 70812

Score = 155 bits (78), Expect = 5e-35  
Identities = 129/145 (88%), Gaps = 5/145 (3%)  
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtcctgtggcct-gctggtcaggatcctctgtggct-ccagggg 644  
|||||  
Sbjct: 47586 tggttctctgtgtgtccagcctggtcctag-tggtcaggatcctctgtggatcccagaag 47528

Query: 645 tctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704  
|||||  
Sbjct: 47527 -atgccgctgaccaggctgtacatgaccat-ctgctcacagtgctgggtcttcctcctctg 47470

Query: 705 cggcctgccctttggcattcagtg 729  
|||||  
Sbjct: 47469 cggcctgcccattggcattcagtg 47445

Score = 147 bits (74), Expect = 1e-32  
Identities = 120/135 (88%), Gaps = 2/135 (1%)  
Strand = Plus / Minus

Query: 591 tctctgtgggtccagtcctggccctgctggtcaggatcctctgtgggtccaggg-gtctgc 649  
|||||  
Sbjct: 93195 tctctgtgggtccagcctggctcctgctggtcaggatcctttgtgggtcccgaaga-tgc 93137

Query: 650 cactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgcggcc 709  
|||||  
Sbjct: 93136 cactgaccaggctgtacgtgaccatcctgctcatagcgctgggtcttcctcctctgtggcc 93077

Query: 710 tgccctttggcattc 724  
|||||  
Sbjct: 93076 tgccctttggcattc 93062

Score = 145 bits (73), Expect = 5e-32  
Identities = 132/151 (87%), Gaps = 4/151 (2%)  
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtcctggccctgctggtcaggatcctctgtgggtccagg-ggt 645  
|||||  
Sbjct: 691 tggttctctgcgggtccagcccggctcctgctggtcaggatcctttgtggatcccgaag- 633

Query: 646 ctgccac-tgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704  
|||||  
Sbjct: 632 atgcc-cttgaccaggctgtacatgaccatcctgctcacagtgctgggtcttcctcctctg 574

Query: 705 cggcctgcccttttggcattcagtggttccta 735  
| |||||  
Sbjct: 573 tgacctgcccttttggcattcagtgattccta 543

Score = 119 bits (60), Expect = 3e-24  
Identities = 128/150 (85%), Gaps = 4/150 (2%)  
Strand = Plus / Minus

Query: 106 ctgacaccttttcattgccctggcggttaggaaacg-ggtttgtgctctggctcct 164  
| |||||  
Sbjct: 24568 ctgacacctcatcattgacctggcggttagcaggaaatgcag-tcatgctctggctcct 24510

Query: 165 gggcttccgcatgcgcaggaacgccttctctgtctacgtcctcagcctggccggggccga 224  
| |||||  
Sbjct: 24509 gggcttctgcatgcacagtaacaccttctctctacatcctcaacctggccagggtga 24450

Query: 225 ctctcctcttc-ctctgcttccagattataa 253  
| |||||  
Sbjct: 24449 ctctcctctgcac-ctgcttccagattataa 24421

Score = 119 bits (60), Expect = 3e-24  
Identities = 91/101 (90%), Gaps = 2/101 (1%)  
Strand = Plus / Minus

Query: 138 aggaaacg-ggtttgtgctctggctcctgggcttccgcatgcgcaggaacgccttctctg 196  
| |||||  
Sbjct: 109327 aggaaacgcgg-ttgtgctctggctcctgggcttccgcatgcgcaggaacgccgtctcca 109269

Query: 197 tctacgtcctcagcctggccggggccgacttctcttctc 237  
| |||||  
Sbjct: 109268 tctacatcctcaacctggctgcgcagacttctcttctc 109228

Score = 111 bits (56), Expect = 7e-22  
Identities = 102/117 (87%), Gaps = 2/117 (1%)  
Strand = Plus / Minus

Query: 122 ccctggctcgggctggtaggaaacg-ggtttgtgctctggctcctgggcttccgcatgcgc 180  
| |||||  
Sbjct: 71425 cccttgctcgggctgacaggaaacgcag-ttgtgctctggctcctgggctgccgcatgcgc 71367

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctc 237  
| |||||  
Sbjct: 71366 aggaacgccttctccatctacatcctcaacttggccgcagacttctcttctc 71310



```
Query: 587      tggttctctgtgggtccagtcctggccctgctggtcaggatcctctgtgggtcc-agggggt 645
                |||||
Sbjct: 24083    tggttctctgtgggtccaccctggcctgctgtgcaggatcatatgtggatcccagaaga 24024
```

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705  
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 Sbjct: 24023 -tgccgctgaccaggctgtatgtgaccatcctgctcacagggtggtcttcctcttctgc 23965

Query: 706    ggccctgccctttggcattcagtggttcctaata-tggatctg-gaaggatt 757  
              ||||||| | ||||||| ||||| ||| | ||||| | |||||  
Sbjct: 23964    agcctgccctcagcattcagtgattcctattat-actggatc-gagaaggatt 23913

Score = 109 bits (55), Expect = 3e-21  
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Strand = Plus / Minus

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               |||||
Sbjct: 108888   tggttctctgtgggtccagcctggctcctgctgattaggattctctgtggatcctggaag- 108830
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Query: 646      ctgccactgaccaggctgtacctgaccatcctgctcacagtgctggtgttcctcctctgc 705
               ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 108829   atgcctctgaccgggctgtacgtgacgatcctgctcacagtgctagtcttcctactccgc 108770

```

```
Query: 706      ggcctgccctttggcattcagtgg 729
              |||||
Sbjct: 108769  agcctgcccttcggcattcggtgg 108746
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Score = 101 bits (51), Expect = 7e-19  
Identities = 75/83 (90%)  
Strand = Plus / Minus

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Query: 151      gtgctctggctcctgggcttccgcatgcgaggaaacgccttctctgtctacgtcctcagc 210
               |||
Sbjct: 93625    gtgctctggctcctgggcttccgcatgcgaggaaacgccttctccatctacatcttcaac 93566
```

```
Query: 211   ctggccggggccgacttctctt 233
           ||| || |||||
Sbjct: 93565 ctgtccatggccgacttctctt 93543
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Score = 95.6 bits (48), Expect = 4e-17

Identities = 89/102 (87%), Gaps = 4/102 (3%)  
Strand = Plus / Minus

```
Query: 138   aggaaacg-ggtttgtgctctggctcctgggcttccgcattgcgcaggaacgcct-tctct 195
            ||||| | | ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 48021 aggaaacgcgg-ttgtgctctggctcctgggcttccgcattgtgcaggaacgc-tgtctcc 47964
```

```
Query: 196   gtctacgtcctcagcctggccggggccgacttcctcttctc 237
           ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 47963 atctacatcctcaacctggctcgggccaacttcctcctctc 47922
```

Score = 83.8 bits (42), Expect = 2e-13  
Identities = 83/96 (86%), Gaps = 3/96 (3%)  
Strand = Plus / Minus

Query: 154 ctctggctcctgggcttcgcgatgcgaggaacgccttctctgtctacgtcctcagcctg 213  
|||||  
Sbjct: 1107 ctctggctcctgggatttcgcgctgcacaggaacaccttctccctctacaccctcaacctg 1048

```
Query: 214   gccggggccgacttcctcttctctgcttccagatt 249
           |||||
Sbjct: 1047 gccggggccgacttc-t-t-cctctgctcccagatt 1015
```

```
>AC107948.7.1.156839
      Length = 156839
```

Score = 216 bits (109), Expect = 2e-53  
Identities = 195/223 (87%), Gaps = 4/223 (1%)  
Strand = Plus / Minus

```
Query: 320      ctgtgatgacctgtgcctaccttgcaggcctgagcatgctgagcaccgtcagcaccgagc 379
               ||| ||||| ||| | ||||| || ||||| ||| ||||| ||| ||||| |||
Sbjct: 155761   ctgtgatgacctttccctactttacaggcctgagtatgctgagcgccatcagcaccgagc 155702
```

Query: 380 gctgctgtccgtcctgtggcccatctggtatcgctgccgccgccccagacacctgtcag 439  
 |||||  
 Sbjct: 155701 gctgctgtctgttctgtggcccatctggtaccgtgccgccgccccacacacctgtcag 155642

Query: 440 cggtcggtgtgtgtcctgctctgggccctgtccctactgctgagcat-cttggaag-ggaa 497  
 |||||  
 Sbjct: 155641 cggtcggtgtgtgtcctgctctgggccctgtccctgctgtttagatgct-gga-gtggag 155584

```
Query: 498      gttctgtggcttcttatttagtgatggtgactctggttggtgt 540
               ||||| ||| | ||||| || ||| ||| |||||
Sbjct: 155583  gttctgtgacttctgtttagtggtgctgattctagttggtgt 155541
```

gcat

cgctg

tact

gttg

gtgg

gtgt

etcct

Query: 175 atgcgaggaacgcct-tctctgtctacgtcctcagcctggccggggccgacttcctctt 233  
|||||  
Sbjct: 155894 atgcgaggaacg-ctgtctccatctacatcctcaacctggccgcagcagacttcctctt 155836

Query: 234 cctctgcttcagattata 252  
|||||  
Sbjct: 155835 cctcagcttcagattata 155817

Score = 89.7 bits (45), Expect = 3e-15  
Identities = 123/148 (83%), Gaps = 5/148 (3%)  
Strand = Plus / Minus

Query: 668 tgaccatcctgctcacagtgtgtgttcctcctctgcggcctgccctttggcattcagt 727  
|||||  
Sbjct: 132286 tgaccatcctgctcacagtgtgtgttcctccttatttgcagcctgcccttaggcattaagt 132227

Query: 728 gggttcctaataattatggatc-tggaaggattctgatgtcttattttggcatatt-catcc 785  
|||||  
Sbjct: 132226 gggttcctattattctggatcctcgt-ggattttgatatcttcctttgtcat-ttgcaacc 132169

Query: 786 aagtttcagttgtcctgtcatctcttaa 813  
| |||||  
Sbjct: 132168 a-gtttcagatgtcctgtcctctcttaa 132142

>AC090099.14.1.172939  
Length = 172939

Score = 216 bits (109), Expect = 2e-53  
Identities = 195/223 (87%), Gaps = 4/223 (1%)  
Strand = Plus / Minus

Query: 320 ctgtgatgacctgtgcctaccttgaggcctgagcatgctgagcaccgtcagcaccgagc 379  
|||||  
Sbjct: 77620 ctgtgatgacctttccctactttacaggcctgagtatgctgagcgccatcagcaccgagc 77561

Query: 380 gctgcctgtccgtcctgtggcccatctggtatcgctgccgccccagacacctgtcag 439  
|||||  
Sbjct: 77560 gctgcctgtctgttctgtggcccatctggtaccgctgccgccccacacacctgtcag 77501

Query: 440 cggtcgtgtgtgtcctgctctgggccctgtccctactgctgagcat-cttggaag-ggaa 497  
|||||  
Sbjct: 77500 cggtcgtgtgtgtcctgctctggggcctgtccctgctgtttagtagtgct-gga-gtggag 77443

Query: 498 gttctgtggcttcttatttagtgatggtgactctggttggtgt 540  
|||||  
Sbjct: 77442 gttctgtgacttcctgttttagtggtgctgattctagttggtgt 77400

Score = 212 bits (107), Expect = 3e-52  
Identities = 231/274 (84%), Gaps = 4/274 (1%)  
Strand = Plus / Minus

Query: 310    ttcttcacca-ctgtgatgacctgtgcctaccttgcaggcctgagcatgctgagcaccgt 368  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 54518   ttcttcaccagc-gtgatgacctttgcctaccttgtaggcctgagcatgctgagtgccat 54460

Query: 369    cagcaccgagcgctgcctgtccgtcctgtggcccatctggtatc-gctgccgccgcccc 427  
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 54459   cagtactgagtgtgcctgtctgtcctgcggcctatctggta-ctgctgctgctgccaa 54401

Query: 428    gacacctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctgagcatct 487  
             || | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 54400   gaaacctgtcaactgtcatgtgtgccctgccctgggccctgtccctgctgctgaacaccc 54341

Query: 488    tggaaggggaagttctgtggcttcttatttagtgatggtgactctggttggtgtcagacat 547  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 54340   tggaaggggaagttttgtggcttcttagttagtaaatggtgactatggttggtgttgacat 54281

Query: 548    ttgatttcatcactgcagcgtggctgattttttt 581  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 54280   ttgatttcatcactgcagtggtggctggnnnnnnn 54247

Score = 200 bits (101), Expect = 1e-48  
Identities = 177/202 (87%), Gaps = 2/202 (0%)  
Strand = Plus / Minus

Query: 320    ctgtgatgacctgtgcctaccttgcaggcctgagcatgctgagcaccgtcagcaccgagc 379  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 113674   ctgtgatgacctttccctactttataggcctaagcatgctgagcgccatcagcaccgagc 113615

Query: 380    gctgcctgtccgtcctgtggcccatctggtatcgctgccgccgccccagacacctgtcag 439  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 113614   gctgcctgtccatcctgtggcccatctggtaccactgccgccgccccagataacctgtcat 113555

Query: 440    cggtcgtgtgtgtcctgctctgggccctgtccctactgctgagcatcttggaag-ggaag 498  
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 113554   cagtcatgtgtgtcctgctctgggccctgtccctgctgcggagtatcctgga-gtggatg 113496

Query: 499    ttctgtggcttcttatttagtg 520  
             ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 113495   ttctgtgacttcctgtttagtg 113474

Score = 172 bits (87), Expect = 2e-40  
Identities = 130/144 (90%), Gaps = 2/144 (1%)  
Strand = Plus / Minus

```
Query: 587      tggttctctgtgggtccagtcctggccctgctggtcaggatcctctgtggctccaggg-gt 645
               |||||
Sbjct: 113407  tggttctctgtgggtccagcctggctcctgctggtcaggattctctgtggatcccgggaaga 113348
```

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705  
Sbjct: 113347 -tgccgctgaccaggctgtacgtgaccatcctcctcacagtgctgggtcttcctcctctgt 113289

```
Query: 706      ggcctgccctttggcattcagtg 729
              |||||
Sbjct: 113288  ggcctgccctttggcattcagtg 113265
```

Score = 163 bits (82), Expect = 2e-37  
Identities = 125/139 (89%), Gaps = 2/139 (1%)  
Strand = Plus / Minus

```
Query: 587      tggttctctgtggtccagtcctggccctgctggtcaggatcctctgtggctccagg-ggt 645
                |||||   |||| | ||| ||||||||| ||||||| ||| |||
Sbjct: 77353    tggttctctgtgtttccagcctggtcctgctggtcaggatcctctgtggatcccgaag- 77295
```

```

Query: 646      ctgccactgaccaggctgtacctgaccatcctgctcacagtgcctgggtgttcctcctctgc 705
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 77294    atgccgctgaccaggctgtacgtgaccatcctgctcacagtgcctgggtcttcctcctctgc 77235

```

```
Query: 706      ggctgccccttgccattc 724
               |||||
Sbjct: 77234    ggctgccccttcggcattc 77216
```

Score = 159 bits (80), Expect = 3e-36  
Identities = 172/202 (85%), Gaps = 4/202 (1%)  
Strand = Plus / Minus

```
Query: 280      ttctgttccatctccatc-aatttccctagcttcttccaccactgtgatga-cctgtgcct 337
               ||||| ||||| ||||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 97620    ttctcttccatctccatctacttt-cctagcttcttcaatgctgtgatgatcct-ttcct 97563
```

```
Query: 338      accttgaggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgt 397
               |||||
Sbjct: 97562    accttgagggctgagcatgctaagcaccatcagcatcaaacactgcataatctgccctgt 97503
```

Query: 398 ggcccatctggtatcgctgccgcccagacacctgtcagcggtcgtgtgtgcctgc 457  
 |||||  
 Sbjct: 97502 ggcccatctggtaccactgccgtcgccccacacacctgtcagcagtcctgtgtgccctgc 97443

Query: 458 tctgggcccctgtccctactgct 479  
|||||  
Sbjct: 97442 tctgggccccgtccctgctgct 97421

Score = 139 bits (70), Expect = 3e-30  
Identities = 191/230 (83%), Gaps = 8/230 (3%)  
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtctggccctgctggtcaggatcctctgtggctcc-agggg 645  
|||||  
Sbjct: 97313 tggttctctgtgggtccaacctggttctgctagtcaggatcctctgtggctcccagcaga 97254

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705  
|||||  
Sbjct: 97253 -tgccactgagcgggctgtagatgaccatcttgctcacagtgctgggtgtttctcctatgc 97195

Query: 706 ggccctgccctttggcattcagtggttcctaataattatggatctggaagga-ttctgatgt 764  
|||||  
Sbjct: 97194 agcctgccccttggcattcagtgattcctgttattctgga-ctgaaaaaactt-tcatgt 97137

Query: 765 cttatatttggcatattcatccaagtttcagttgtcctg-tcatctcttaa 813  
|||  
Sbjct: 97136 cttcctttgtcatgttcttcca-gtttcagttgtc-tggtcctctcttaa 97089

Score = 129 bits (65), Expect = 3e-27  
Identities = 121/139 (87%), Gaps = 4/139 (2%)  
Strand = Plus / Minus

Query: 116 tcattgccctgggtcgggctggtaggaaacg-ggtttgtgctctggctcctgggcttccgc 174  
|||||  
Sbjct: 77812 tcatttcccttgtcggactgacaggaaacgcgg-ttgtgctctggctcctgggctaccgc 77754

Query: 175 atgcgaggaacgcct-tctctgtctacgtcctcagcctggccggggccgacttcctctt 233  
|||||  
Sbjct: 77753 atgcgaggaacg-ctgtctccatctacatcctcaacctggccgcagcagacttcctctt 77695

Query: 234 cctctgcttccagattata 252  
|||  
Sbjct: 77694 cctcagcttccagattata 77676

Score = 109 bits (55), Expect = 3e-21  
Identities = 90/101 (89%), Gaps = 4/101 (3%)  
Strand = Plus / Minus

```
Query: 196      gtctacgtcctcagcctggccggggccgacttctcttct 236
               ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 113786  atctacatcctcaacctggctcgcgcccgacttctcttct 113746
```

```
Query: 668      tgaccatcctgctcacagtgctggtgttcctcctctgcggcctgccctttggcattcagt 727
               ||||||||||||||||||||| ||||| | ||| ||||||||||| ||||| |||
Sbjct: 54149    tgaccatcctgctcacagtgctgctcttccttatttgcagcctgcccttaggcattaagt 54090
```

```

Query: 728      ggttcctaataattatggatc-tggaaggattctgatgtcttattttggcatatt-catcc 785
               |||||
Sbjct: 54089    ggttcctattattctggatcctcgt-ggattttgatatacttcctttgtcat-ttgaacc 54032

```

```
Query: 786      aagtttcagttgtcctgtcatctcttaa 813
              | ||||| ||||| ||||| ||||| |||||
Sbjct: 54031    a-gtttcagatgtcctgtcctctcttaa 54005
```

Score = 81.8 bits (41), Expect = 6e-13  
Identities = 50/53 (94%)  
Strand = Plus / Minus

```

Query: 587      tggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtggctcc 639
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 54228    tggttctctgtgagtcagcctgggtcctgctgggtcaggatcctctgtggctcc 54176

```

```
>AC103974.6.1.189230
      Length = 189230
```

Score = 212 bits (107), Expect = 3e-52  
Identities = 214/249 (85%), Gaps = 4/249 (1%)  
Strand = Plus / Plus

```
Query: 313      ttcaccactgtgatgacctgtgc-ctaccttgaggcctgagcatgctgagcacccgtcag 371
                |||
Sbjct: 17860    ttcaccactgtgatgacct-ttctctactttacaggcctgagcatgctgggctccatcag 17918
```

```
Query: 372   caccgagcgtgcctgtccgtcctgtggcccatctggtatcgctgccgccgcccagaca 431
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 17919 caccaagcactgcctgtccatcctgtggcccatctagtagcgctgccaccacccacaca 17978
```



Query: 432 cctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctgagcatcttgga 491

Query: 492 aggggaagttctgtggcttcttatttagtgatggtgactctgggttggtgtcagacatttga 551

Query: 552      tttcatcac    560  
                 |||||

Score = 145 bits (73), Expect = 5e-32  
Identities = 132/151 (87%), Gaps = 4/151 (2%)  
Strand = Plus / Plus

Query: 587      tggttctctgtgggtccagtctggccctgctggtcaggatcctctgtggctccagg-ggt 645

Query: 646 ctgccac-tgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704

Query: 705 cggcctgccctttggcattcagtggttccta 735

Score = 91.7 bits (46), Expect = 6e-16  
Identities = 84/96 (87%), Gaps = 3/96 (3%)  
Strand = Plus / Plus

Query: 154 ctctggctcctgggcttccgcattgctgaggaacgccttctctgtctacgtcctcagcctg 213

Query: 214 gccggggccgacttcctcttcctctgcttccagatt 249

Database: Homo\_sapiens.latestgp.masked.fa  
 Posted date: Apr 17, 2003 4:52 PM  
 Number of letters in database: 200,810,911,373  
 Number of sequences in database: 33,840

Lambda            K            H

1.37 0.711 1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 0, Extension: 0

Number of Hits to DB: 0

length of query: 1628

length of database: 200,810,911,373

effective HSP length: 21

effective length of query: 792

effective search space used: 0

T: 0

A: 0

X1: 0 ( 0.0 bits)

X2: 20 (39.6 bits)

S1: 12 (24.3 bits)

S2: 38 (75.8 bits)

## EXHIBIT "C"

>NM\_054030 ACCESSION:NM\_054030 NID: gi 16876450 ref NM\_054030.1 Homo sapiens  
G protein-coupled receptor MRGX2 (MRGX2), mRNA  
Length = 993

Score = 1536 bits (775), Expect = 0.0  
Identities = 804/813 (98%), Gaps = 1/813 (0%)  
Strand = Plus / Plus

Query: 1 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60  
|||||  
Sbjct: 1 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60

Query: 61 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120  
|||||  
Sbjct: 61 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120

Query: 121 gccctggtcgggctggttaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180  
|||||  
Sbjct: 121 gccctggtcgggctggttaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240  
|||||  
Sbjct: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240

Query: 241 ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300  
|||||  
Sbjct: 241 ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300

Query: 301 ttccctagcttcttcaccactgtgatgacctgtgcctaccttgccaggcctgagcatgctg 360  
|||||  
Sbjct: 301 ttccctagcttcttcaccactgtgatgacctgtgcctaccttgccaggcctgagcatgctg 360

Query: 361 agcacgcgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420  
|||||  
Sbjct: 361 agcacgcgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420

Query: 421 cgccccagacacctgtcagcggtcggtgtgtgtctctgctctgggccctgtccctactgctg 480  
|||||  
Sbjct: 421 cgccccagacacctgtcagcggtcggtgtgtgtctctgctctgggccctgtccctactgctg 480

Query: 481 agcatcttgaagggaagtctgtggcttcttatttagtgatggtgactctggttggtgt 540  
|||||  
Sbjct: 481 agcatcttgaagggaagtctgtggcttcttatttagtgatggtgactctggttggtgt 540

Query: 541 cagacatttgatttcatcactgcagcggtggctgannnnnnnattcatggttctctgtggg 600  
|||||  
Sbjct: 541 cagacatttgatttcatcactgcagcggtggctgatttttttattcatggttctctgtggg 600

Query: 601 tccagtctggccctgctgggtcaggatcctctgtggctccaggggtctgccactgaccagg 660



&gt;hGPR\_32\_ORF\_03

Length = 813

Score = 1570 bits (792), Expect = 0.0

Identities = 806/813 (99%)

Strand = Plus / Plus

```
Query: 1   atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60
          |||
Sbjct: 1   atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60

Query: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120
          |||
Sbjct: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120

Query: 121  gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttcgcgatgcgc 180
          |||
Sbjct: 121  gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttcgcgatgcgc 180

Query: 181  aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240
          |||
Sbjct: 181  aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240

Query: 241  ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300
          |||
Sbjct: 241  ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300

Query: 301  ttccctagcttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360
          |||
Sbjct: 301  ttccctagcttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360

Query: 361  agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctgggatcgctgccgc 420
          |||
Sbjct: 361  agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctgggatcgctgccgc 420

Query: 421  cgccccagacacctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctg 480
          |||
Sbjct: 421  cgccccagacacctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctg 480

Query: 481  agcatcttggaagggaagtctctgtggcttcttatttagtgatggtgactctggttggtgt 540
          |||
Sbjct: 481  agcatcttggaagggaagtctctgtggcttcttatttagtgatggtgactctggttggtgt 540

Query: 541  cagacatttgatttcatcactgcagcggtggctgannnnnnnattcatggttctctgtggg 600
          |||
Sbjct: 541  cagacatttgatttcatcactgcagcggtggctgatttttttattcatggttctctgtggg 600

Query: 601  tccagtctggccctgctgggtcaggatcctctgtggctccaggggtctgccactgaccagg 660
          |||
```

Sbjct: 601 tccagtctggccctgctgggtcaggatcctctgtgggtccaggggtctgccactgaccagg 660

Query: 661 ctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgcggtcctgccctttggc 720  
|||||


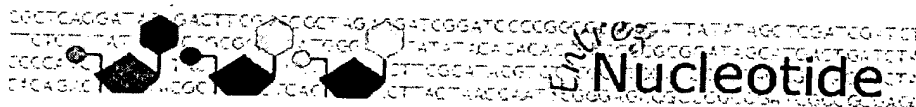
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|||||

Sbjct: 721 attcagtgggttcctaataattatggatctggaaggattctgatgtcttattttggcatatt 780

Query: 781 catccaagtttcagttgtcctgtcatctcttaa 813  
|||||

Sbjct: 781 catccaagtttcagttgtcctgtcatctcttaa 813

[PubMed](#)   [Nucleotide](#)   [Protein](#)   [Genome](#)   [Structure](#)   [PopSet](#)   [Taxonomy](#)   [OMIM](#)   [Bio](#)

Search  for

☐ 1: NM\_054030. Homo sapiens G pr...  
[gi:16876450]

MapView, Related Sequences, Protein, PubMed, Taxonomy,  
LinkOut

LOCUS MRGX2 993 bp mRNA linear PRI 09-FEB-2002  
 DEFINITION Homo sapiens G protein-coupled receptor MRGX2 (MRGX2), mRNA.  
 ACCESSION NM\_054030  
 VERSION NM\_054030.1 GI:16876450  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 993)  
 AUTHORS Dong,X., Han,S., Zylka,M.J., Simon,M.I. and Anderson,D.J.  
 TITLE A diverse family of GPCRs expressed in specific subsets of  
 nociceptive sensory neurons  
 JOURNAL Cell 106 (5), 619-632 (2001)  
 MEDLINE 21435808  
 PUBMED 11551509  
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final  
 NCBI review. The reference sequence was derived from AY042214.1.  
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Score = 1570 bits (792), Expect = 0.0

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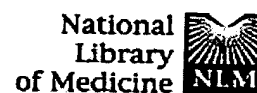
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## A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons.

Dong X, Han S, Zylka MJ, Simon MI, Anderson DJ.

Division of Biology 216-76, California Institute of Technology, Pasadena, CA 91125, USA.

In vertebrates, peripheral chemosensory neurons express large families of G protein-coupled receptors (GPCRs), reflecting the diversity and specificity of stimuli they detect. However, somatosensory neurons, which respond to chemical, thermal, or mechanical stimuli, are more broadly tuned. Here we describe a family of approximately 50 GPCRs related to Mas1, called mrgs, a subset of which is expressed in specific subpopulations of sensory neurons that detect painful stimuli. The expression patterns of mrgs thus reveal an unexpected degree of molecular diversity among nociceptive neurons. Some of these receptors can be specifically activated in heterologous cells by RFamide neuropeptides such as NPFF and NPAF, which are analgesic in vivo. Thus, mrgs may regulate nociceptor function and/or development, including the sensation or modulation of pain.

PMID: 11551509 [PubMed - indexed for MEDLINE]

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